

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANTS: Wallner, Barbara P.
Cooper, Kevin D.

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(ii) TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen Presenting Cell Driven Skin Conditions Using Inhibitors of the CD2/LFA-3 Interaction

(iii) NUMBER OF SEQUENCES: 8

15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: LAHIVE & COCKFIELD
- (B) STREET: 60 State Street, Suite 510
- (C) CITY: Boston
- (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02109-1875

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(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

30

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US92/08755
~~(B) FILING DATE: 06-OCT-1992~~

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(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/862,022
 (B) FILING DATE: 12-APR-1992

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(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/770,969
(B) FILING DATE: 07-OCT-1991

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(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Myers, Louis (PLM)
 (B) REGISTRATION NUMBER: 35,965
 (C) REFERENCE/DOCKET NUMBER: BGP-111CP

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(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

55 (2) INFORMATION FOR SEO ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..750

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(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..84

15

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 85..750

20

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..750
(D) OTHER INFORMATION: /note= "Human transmembrane LFA-3"

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(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 646
(D) OTHER INFORMATION: /note= "Transmembrane domain"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG 48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-28 -25 -20 -15

35

GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA 96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 1

40

ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT 144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

45

GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA 192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

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GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG 240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

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GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA 288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT 336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

005021 5406250

ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA 384
 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 85 90 95 100

5 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA 432
 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 105 110 115

10 CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT 480
 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 120 125 130

15 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG 528
 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 135 140 145

20 ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA 576
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160

TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC 624
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180

25 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA 672
 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 185 190 195

30 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATT CTG AAA TGT 720
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
 200 205 210

35 GAC AGA AAA CCA GAC AGA ACC AAC TCC AAT TGA 753
 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
 215 220

(2) INFORMATION FOR SEQ ID NO:2:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

50 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 -28 -25 -20 -15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 -10 -5 1

55 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 5 10 15 20

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 25 30 35

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 40 45 50
 5 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 55 60 65
 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 70 75 80
 10 Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 85 90 95 100
 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 15 105 110 115
 Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 120 125 130
 20 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
 135 140 145
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160
 25 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180
 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 30 185 190 195
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
 200 205 210
 35 Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
 215 220

(2) INFORMATION FOR SEQ ID NO:3:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- 50 (A) NAME/KEY: CDS
- (B) LOCATION: 1..720
- (ix) FEATURE:
- 55 (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..84
- (ix) FEATURE:
- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 85..720

005007 5906253

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..720

5 (D) OTHER INFORMATION: /note= "Human PI-linked LFA-3"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 568..720

10 (D) OTHER INFORMATION: /note= "Signal sequence for
PI-linkage"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG 48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-28 -25 -20 -15

20 GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA 96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 1

25 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT 144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

30 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA 192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG 240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

35 GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA 288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

40 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT 336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

45 ACC ATG AAG TTC TTT CTT TAT GTG CTT GAG TCT CTT CCA TCT CCC ACA 384
Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
85 90 95 100

50 CTA ACT TGT GCA TTG ACT AAT GGA AGC ATT GAA GTC CAA TGC ATG ATA 432
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
105 110 115

CCA GAG CAT TAC AAC AGC CAT CGA GGA CTT ATA ATG TAC TCA TGG GAT 480
Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
120 125 130

55 TGT CCT ATG GAG CAA TGT AAA CGT AAC TCA ACC AGT ATA TAT TTT AAG 528
Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
135 140 145

0030465 5940E260

ATG GAA AAT GAT CTT CCA CAA AAA ATA CAG TGT ACT CTT AGC AAT CCA 576
 Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
 150 155 160

5 TTA TTT AAT ACA ACA TCA TCA ATC ATT TTG ACA ACC TGT ATC CCA AGC 624
 Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
 165 170 175 180

10 AGC GGT CAT TCA AGA CAC AGA TAT GCA CTT ATA CCC ATA CCA TTA GCA 672
 Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
 185 190 195

15 GTA ATT ACA ACA TGT ATT GTG CTG TAT ATG AAT GGT ATG TAT GCT TTT 720
 Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
 200 205 210

TAA 723

20 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 -28 -25 -20 -15

35 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 -10 -5 1

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 5 10 15 20

40 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 25 30 35

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 40 45 50

45 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 55 60 65

50 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 70 75 80

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
 85 90 95 100

55 Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
 105 110 115

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
 120 125 130

09730465 130500

-5

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5	ACC TGG GGT GCC TTG GGT CAG GAC ATC AAC TTG GAC ATT CCT AGT TTT Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe	144
	10 15 20	
10	CAA ATG AGT GAT GAT ATT GAC GAT ATA AAA TGG GAA AAA ACT TCA GAC Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp	192
	25 30 35 40	
15	AAG AAA AAG ATT GCA CAA TTC AGA AAA GAG AAA GAG ACT TTC AAG GAA Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu	240
	45 50 55	
20	AAA GAT ACA TAT AAG CTA TTT AAA AAT GGA ACT CTG AAA ATT AAG CAT Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His	288
	60 65 70	
25	CTG AAG ACC GAT GAT CAG GAT ATC TAC AAG GTA TCA ATA TAT GAT ACA Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr	336
	75 80 85	
30	AAA GGA AAA AAT GTG TTG GAA AAA ATA TTT GAT TTG AAG ATT CAA GAG Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu	384
	90 95 100	
35	AGG GTC TCA AAA CCA AAG ATC TCC TGG ACT TGT ATC AAC ACA ACC CTG Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu	432
	105 110 115 120	
40	ACC TGT GAG GTA ATG AAT GGA ACT GAC CCC GAA TTA AAC CTG TAT CAA Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln	480
	125 130 135	
45	GAT GGG AAA CAT CTA AAA CTT TCT CAG AGG GTC ATC ACA CAC AAG TGG Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp	528
	140 145 150	
50	ACC ACC AGC CTG AGT GCA AAA TTC AAG TGC ACA GCA GGG AAC AAA GTC Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val	576
	155 160 165	
55	AGC AAG GAA TCC AGT GTC GAG CCT GTC AGC TGT CCA GAG AAA GGT CTG Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu	624
	170 175 180	
60	GAC ATC TAT CTC ATC ATT GGC ATA TGT GGA GGA GGC AGC CTC TTG ATG Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met	672
	185 190 195 200	
65	GTC TTT GTG GCA CTG CTC GTT TTC TAT ATC ACC AAA AGG AAA AAA CAG Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln	720
	205 210 215	
70	AGG AGT CGG AGA AAT GAT GAG GAG CTG GAG ACA AGA GCC CAC AGA GTA Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val	768
	220 225 230	
75	GCT ACT GAA GAA AGG GGC CGG AAG CCC CAC CAA ATT CCA GCT TCA ACC	816

00503F 5940E260

	Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr	
	235 240 245	
5	CCT CAG AAT CCA GCA ACT TCC CAA CAT CCT CCT CCA CCA CCT GGT CAT Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His	864
	250 255 260	
10	CGT TCC CAG GCA CCT AGT CAT CGT CCC CCG CCT CCT GGA CAC CGT GTT Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val	912
	265 270 275 280	
15	CAG CAC CAG CCT CAG AAG AGG CCT CCT GCT CCG TCG GGC ACA CAA GTT Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val	960
	285 290 295	
	CAC CAG CAG AAA GGC CCG CCC CTC CCC AGA CCT CGA GTT CAG CCA AAA His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys	1008
	300 305 310	
20	CCT CCC CAT GGG GCA GCA GAA AAC TCA TTG TCC CCT TCC TCT AAT Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn	1053
	315 320 325	
25	TAA	1056
	(2) INFORMATION FOR SEQ ID NO:6:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
40	Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn -24 -20 -15 -10	
	Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu -5 1 5	
45	Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe 10 15 20	
	Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp 25 30 35 40	
50	Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu 45 50 55	
55	Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His 60 65 70	
	Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr 75 80 85	
	Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu	

005001 " 5406250

90 95 100

Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
105 110 115 120

5 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
125 130 135

10 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
140 145 150

Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
155 160 165

15 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
170 175 180

Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
185 190 195 200

20 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
205 210 215

Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
220 225 230

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
235 240 245

30 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
250 255 260

Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
265 270 275 280

35 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
285 290 295

His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
300 305 310

Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
315 320 325

45 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1041

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..84

5 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 85..1041

10 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 85..1041
 (D) OTHER INFORMATION: /note- "LFA3TIP"

15 (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 360..361
 (D) OTHER INFORMATION: /note- "LFA-3/IgG fusion point"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GTT GCT GGG AGC GAC GCG GGG CGG GCC CTG GGG GTC CTC AGC GTG	48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val	
-28 -25 -20 -15	
25 GTC TGC CTG CTG CAC TGC TTT GGT TTC ATC AGC TGT TTT TCC CAA CAA	96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln	
-10 -5 1	
30 ATA TAT GGT GTT GTG TAT GGG AAT GTA ACT TTC CAT GTA CCA AGC AAT	144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn	
5 10 15 20	
35 GTG CCT TTA AAA GAG GTC CTA TGG AAA AAA CAA AAG GAT AAA GTT GCA	192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala	
25 30 35	
40 GAA CTG GAA AAT TCT GAA TTC AGA GCT TTC TCA TCT TTT AAA AAT AGG	240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg	
40 45 50	
GTT TAT TTA GAC ACT GTG TCA GGT AGC CTC ACT ATC TAC AAC TTA ACA	288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr	
55 60 65	
45 TCA TCA GAT GAA GAT GAG TAT GAA ATG GAA TCG CCA AAT ATT ACT GAT	336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp	
70 75 80	
50 ACC ATG AAG TTC TTT CTT TAT GTC GAC AAA ACT CAC ACA TGC CCA CCG	384
Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro	
85 90 95 100	
55 TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC	432
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro	
105 110 115	
CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA	480
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr	

	120	125	130	
5	TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn 135 140 145	528		
10	TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg 150 155 160	576		
15	GAG GAG CAG TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val 165 170 175 180	624		
20	CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser 185 190 195	672		
25	AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys 200 205 210	720		
30	GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp 215 220 225	768		
35	GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe 230 235 240	816		
40	TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu 245 250 255 260	864		
45	AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe 265 270 275	912		
50	TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly 280 285 290	960		
55	AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr 295 300 305	1008		
60	ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGAGTGCGG Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 310 315	1050		

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 347 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 -28 -25 -20 -15
 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 -10 -5 1
 10 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 5 10 15 20
 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
 25 30 35
 15 Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
 40 45 50
 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
 20 55 60 65
 Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
 70 75 80
 25 Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro
 85 90 95 100
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 105 110 115
 30 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 120 125 130
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 135 140 145
 35 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 150 155 160
 40 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 165 170 175 180
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 185 190 195
 45 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 200 205 210
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 215 220 225
 50 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 230 235 240
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 245 250 255 260
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 265 270 275

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
280 285 290

5 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 295 300 305

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
310 315

Age	Sex	Height	Weight	Body Mass Index	Waist Circumference	Waist-Hip Ratio	Trunk Fat (%)	Visceral Fat (cm ³)	Subcutaneous Fat (cm ³)	Visceral Fat Index	Subcutaneous Fat Index	Visceral Fat to Subcutaneous Fat Ratio
20	M	170	65	22.3	85	0.91	15	100	200	0.05	0.10	0.5
25	F	160	55	21.5	75	0.88	12	80	180	0.04	0.09	0.4
30	M	175	75	24.5	95	0.93	18	120	250	0.06	0.12	0.5
35	F	165	65	23.8	85	0.90	14	90	200	0.05	0.10	0.5
40	M	180	85	26.2	105	0.95	20	140	300	0.07	0.14	0.5
45	F	170	75	25.9	95	0.92	16	110	250	0.06	0.12	0.5
50	M	185	95	28.5	115	0.97	22	160	350	0.08	0.16	0.5
55	F	175	85	27.9	105	0.94	18	130	300	0.07	0.14	0.5
60	M	190	105	30.0	125	0.99	24	180	400	0.09	0.18	0.5
65	F	180	95	29.2	115	0.96	20	150	350	0.08	0.16	0.5
70	M	195	115	31.5	135	1.01	26	200	450	0.10	0.20	0.5
75	F	185	105	31.0	125	0.98	22	170	400	0.09	0.18	0.5
80	M	200	125	31.3	145	1.03	28	220	500	0.11	0.22	0.5
85	F	190	115	31.6	135	1.00	24	190	450	0.10	0.20	0.5
90	M	205	135	32.0	155	1.05	30	240	550	0.12	0.24	0.5
95	F	195	125	32.0	145	1.02	26	210	500	0.11	0.22	0.5
100	M	210	145	32.7	165	1.07	32	260	600	0.13	0.26	0.5
105	F	200	135	33.8	155	1.04	28	230	550	0.12	0.24	0.5
110	M	215	155	33.5	175	1.09	34	280	650	0.14	0.28	0.5
115	F	205	145	34.6	165	1.06	30	250	600	0.13	0.26	0.5
120	M	220	165	34.5	185	1.11	36	300	700	0.15	0.30	0.5
125	F	210	155	35.2	175	1.08	32	270	650	0.14	0.28	0.5
130	M	225	175	34.2	195	1.13	38	320	750	0.16	0.32	0.5
135	F	215	165	35.8	185	1.10	34	290	700	0.15	0.30	0.5
140	M	230	185	35.5	205	1.15	40	340	800	0.17	0.34	0.5
145	F	220	175	36.2	195	1.12	36	310	750	0.16	0.32	0.5
150	M	235	195	35.8	215	1.17	42	360	850	0.18	0.36	0.5
155	F	225	185	36.8	205	1.14	38	330	800	0.17	0.34	0.5
160	M	240	205	35.8	225	1.19	44	380	900	0.19	0.38	0.5
165	F	230	195	37.4	215	1.16	40	350	850	0.18	0.36	0.5
170	M	245	215	35.5	235	1.21	46	400	950	0.20	0.40	0.5
175	F	235	205	38.0	225	1.18	42	370	900	0.19	0.38	0.5